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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/996,569

DATE: 12/06/2001

TIME: 15:04:44

Input Set : A:\PF201D2-SeqList-text.txt

Output Set: N:\CRF3\12062001\I996569.raw

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3 <110> APPLICANT: Soppet et al.
 5 <120> TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
 7 <130> FILE REFERENCE: PF201D1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/996,569
 C--> 10 <141> CURRENT FILING DATE: 2001-11-30
 12 <150> PRIOR APPLICATION NUMBER: 08/468,011
 13 <151> PRIOR FILING DATE: 1995-06-06
 15 <160> NUMBER OF SEQ ID NOS: 28
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2003
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
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 26 <222> LOCATION: (90)..(1715)
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 31 cccctgcttct tcctacagcc gttccgggc atg gcc tgg ctg ggg gcg tcg ctc 113
 32 Met Ala Trp Leu Gly Ala Ser Leu
 33 1 5
 35 cac gtc tgg ggt tgg cta atg ctc ggc agc tgc ctc ctg gcc aga gcc 161
 36 His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
 37 10 15 20
 39 cag ctg gat tct gat ggc acc atc act ata gag gag cag att gtc ctt 209
 40 Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
 41 25 30 35 40
 43 gtg ctg aaa gcg aaa gta caa tgt gaa ctc aac atc aca gct caa ctc 257
 44 Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
 45 45 50 55
 47 cag gag gga gaa ggt aat tgt ttc cct gaa tgg gat gga ctc att tgt 305
 48 Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
 49 60 65 70
 51 tgg ccc aga gga aca gtg ggg aaa ata tcg gct gtt cca tgc cct cct 353
 52 Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
 53 75 80 85
 55 tat att tat gac ttc aac cat aaa gga gtt gct ttc cga cac tgt aac 401
 56 Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
 57 90 95 100
 59 ccc aat gga aca tgg gat ttt atg cac agc tta aat aaa aca tgg gcc 449
 60 Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
 61 105 110 115 120
 63 aat tat tca gac tgc ctt cgc ttt ctg cag cca gat atc agc ata gga 497
 64 Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
 65 125 130 135
 67 aag caa gaa ttc tgt gaa cgc ctc tat gta atg tat acc gtt gcc tac 545
 68 Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr

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69		140		145		150	
71	tcc atc tct ttt ggt tcc ttg gct gtg gct att ctc atc att ggt tac	593					
72	Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr						
73		155		160		165	
75	ttc aga cga ttg cat tgc act agg aac tat atc cac atg cac tta ttt	641					
76	Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe						
77		170		175		180	
79	gtg tct ttc atg ctg aga gct aca agc atc ttt gtc aaa gac aga gta	689					
80	Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val						
81	185		190		195		200
83	gtc cat gct cac ata gga gta aag gag ctg gag tcc cta ata atg cag	737					
84	Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln						
85		205		210		215	
87	gat gac cca caa aat tcc att gag gca act tct gtg gac aaa tca caa	785					
88	Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln						
89		220		225		230	
91	tat atc ggg tgc aag att gct gtt gtg atg ttt att tac ttc ctg gct	833					
92	Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala						
93		235		240		245	
95	aca aat tat tat tgg atc ctg gtg gaa ggt ctc tac ctg cat aat ctc	881					
96	Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu						
97		250		255		260	
99	atc ttt gtg gct ttc ttt tcg gac acc aaa tac ctg tgg ggc ttc atc	929					
100	Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile						
101	265		270		275		280
103	ttg ata ggc tgg ggg ttt cca gca gca ttt gtt gca gca tgg gct gtg	977					
104	Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val						
105		285		290		295	
107	gca cga gca act ctg gct gat gcg agg tgc tgg gaa ctt agt gct gga	1025					
108	Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly						
109		300		305		310	
111	gac atc aag tgg att tat caa gca ccg atc tta gca gct att ggg ctg	1073					
112	Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu						
113		315		320		325	
115	aat ttt att ctg ttt ctg aat acg gtt aga gtt cta gct acc aaa atc	1121					
116	Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile						
117		330		335		340	
119	tgg gag acc aat gca gtt ggg cat gac aca agg aag caa tac agg aaa	1169					
120	Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys						
121	345		350		355		360
123	ctg gcc aaa tcg aca ctg gtc ctg gtc cta ttt gga gtg cat tac	1217					
124	Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr						
125		365		370		375	
127	atc gtg ttc gtg tgc ctg cct cac tcc ttc act ggg ctc ggg tgg gag	1265					
128	Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu						
129		380		385		390	
131	atc cgc atg cac tgt gag ctc ttc ttc aac tcc ttt cag ggt ttc ttt	1313					
132	Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe						
133		395		400		405	

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135 gtg tct atc atc tac tgc tac tgc aat gga gag gtt cag gca gag gtg 1361
136 Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val
137 410 415 420
139 aag aag atg tgg agt cgg tgg aat ctc tcc gtg gac tgg aaa agg aca 1409
140 Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr
141 425 430 435 440
143 ccg cca tgt ggc agc cgc aga tgc ggc tca gtg ctc acc acc gtg acg 1457
144 Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr
145 445 450 455
147 cac agc acc agc agc cag tca cag gtg gcg gca gca cac gca tgg tgc 1505
148 His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys
149 460 465 470
151 tta tct ctg gca aag ctg cca aga tcg cca gca gac agc ctg aca gcc 1553
152 Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala
153 475 480 485
155 aca tca ctt tac ctg gct atg tct gga gta act cag agc agg act gcc 1601
156 Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
157 490 495 500
159 tca cac act ctc tcc acg agg agc aac aag gaa gat agt ggg agg cag 1649
160 Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
161 505 510 515 520
163 aga gat gat att cta atg gag aag cct tcc agg cct atg gaa tct aac 1697
164 Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
165 525 530 535
167 cca gac act gaa gga tgacaaggag aaactgagga tgttctctga atggacatgt 1752
168 Pro Asp Thr Glu Gly
169 540
171 gtggtgact ttcattgggct ggtccaatgg ctggttggtg gagaggggctt ggctgatact 1812
173 cctatgcttg agcacaagg ctgaaaattc agttaagggtg ttacttaata atagttttta 1872
175 ggctccatga attggctcct gtaaatacta acgacatgaa aatgcaagtg tcaatggagt 1932
177 agtttattac cttctattgg catcaagttt tctctataat taatgtatgg tatttgctct 1992
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185 <211> LENGTH: 541
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187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 2
190 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
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193 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
194 20 25 30
196 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
197 35 40 45
199 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
200 50 55 60
202 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
203 65 70 75 80
205 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
206 85 90 95

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208 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
209          100          105          110
211 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
212          115          120          125
214 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
215          130          135          140
217 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
218 145          150          155          160
220 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
221          165          170          175
223 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
224          180          185          190
226 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
227          195          200          205
229 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu
230          210          215          220
232 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val
233 225          230          235          240
235 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val
236          245          250          255
238 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp
239          260          265          270
241 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala
242          275          280          285
244 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala
245          290          295          300
247 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala
248 305          310          315          320
250 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr
251          325          330          335
253 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His
254          340          345          350
256 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu
257          355          360          365
259 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His
260          370          375          380
262 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe
263 385          390          395          400
265 Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys
266          405          410          415
268 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn
269          420          425          430
271 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys
272          435          440          445
274 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln
275          450          455          460
277 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg
278 465          470          475          480
280 Ser Pro Ala Asp Ser Leu Thr Ala Thr Ser Leu Tyr Leu Ala Met Ser

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281          485          490          495
283 Gly Val Thr Gln Ser Arg Thr Ala Ser His Thr Leu Ser Thr Arg Ser
284          500          505          510
286 Asn Lys Glu Asp Ser Gly Arg Gln Arg Asp Asp Ile Leu Met Glu Lys
287          515          520          525
289 Pro Ser Arg Pro Met Glu Ser Asn Pro Asp Thr Glu Gly
290          530          535          540
294 <210> SEQ ID NO: 3
295 <211> LENGTH: 23
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <221> NAME/KEY: Primer_Bind
301 <223> OTHER INFORMATION: This 5' primer sequence contains a SmaI restriction
302     enzyme site followed by nucleotides corresponding to PTH receptor
303     coding sequence.
306 <400> SEQUENCE: 3
307 cagccgtccc gggcttggcc tgg                                     23
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 27
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <221> NAME/KEY: Primer_Bind
317 <223> OTHER INFORMATION: This 3' primer sequence contains a SalI restriction
318     enzyme site and a sequence complementary to the human PTH
319     receptor.
321 <400> SEQUENCE: 4
322 cctcagtgtc gacttgtcat ccttcag                                     27
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 27
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <221> NAME/KEY: Primer_Bind
332 <223> OTHER INFORMATION: This 5' primer contains a HindIII restriction enzyme site
333     and a nucleotide sequence corresponding to the 5' UTR of the cDNA
334     encoding human PTH receptor.
336 <400> SEQUENCE: 5
337 gttggcatat tggaagcttt ttgcggg                                     27
340 <210> SEQ ID NO: 6
341 <211> LENGTH: 28
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <221> NAME/KEY: Primer_Bind
347 <223> OTHER INFORMATION: This 3' primer sequence contains an XbaI restriction
348     enzyme site, a translation stop codon, and nucleotides
349     complementary to the human PTH receptor coding sequence.

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VERIFICATION SUMMARY

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Input Set : A:\PF201D2-SeqList-text.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date